

41. Moving the next generation of TB diagnostics for drug resistance closer to patients: data sharing

Saturday, 01 November 2014, 09:15 - 11:15

Room 114



Type Symposium

Track TB Bacteriology and Immunology

Topic TB diagnostics and drug susceptibility testing

Description Molecular tools have the potential to increase accuracy, decrease test result turnaround time, and expand access to testing. New high-throughput sequencing technologies require immediate expansion of collaborations across all global partners to develop a unified system and provide wider access to comprehensive data. The NDWG and CPTR are collaborating to accelerate development of new diagnostics by providing a roadmap to comprehensive and standardised genome sequence data that represent the full array of known molecular markers for drug resistance.

Target audience Molecular biologists, microbiologists, laboratory directors, clinicians, programme managers, policy-makers, and donors

Objectives

1. Inform on the next generation of technology for DR detection
2. Inform on the process and requirements for sharing molecular sequence and phenotypic
3. Inform on new standards for quality data
4. Inform on how to share and access data for diagnosis and surveillance
5. Inform on how to infer molecular epidemiological information and transmission from sequence data.

Keywords Tuberculosis; diagnostics; sequencing; standards; data sharing

Coordinator(s) John Ridderhof (USA), Siva Danaviah (South Africa)

Chair(s) Daniela Maria Cirillo (Italy), Nazir Ismail (South Africa)

Presentations

09:15 - 09:30 Requirements for managing "big data": a global database of DR molecular sequence data
Enrique Aviles (USA)

09:35 - 09:50 Overview/intersection of advanced molecular methods and analyses
Stefan Niemann (Germany)

09:55 - 10:10 Genotype and phenotype analysis to understand pathogen success in Mycobacterial strains
Paul Van Helden (South Africa)

10:15 - 10:30 Data standards for interoperability and sharing
Angela Starks (USA)

10:35 - 10:50 A whole genome sequencing approach to investigate the evolution of drug resistance in South Africa
Ruben Van Der Merwe (South Africa)

10:55 - 11:10 Population genomics of the *M. tuberculosis* complex
Sebastien Gagneux (Switzerland)